normalisation methods	scale of C matrix (sc)	scale of T mat	principle	implementation	comparison	
raw counts (none)	☑	☑	no normalisation	base R		
column	☑	☑	normalise based on the sum of counts of each column (sample/cellID)	base R	within-sample	
row	☑	☑	normalise based on the sum of each row (genes/features)	base R	across-sample	
mean	☑	☑	normalise based on the mean of each column(sample/cellID)	base R	within-sample	
column_z-score	☑	☑	centers and scales the columns of a matrix	base R - function scale()	within-sample	
global_z-score	☑	☑	calculated by subtracting the overall average gene abundance from the raw expression for each gene, and dividing that result by the standard deviation (SD) of all of the measured counts across all samples.	base R	across-sample and within-sample	
column_min-max	☐	☑	For every column, the minimum value of that column gets transformed into a 0, the maximum value gets transformed into a 1, and every other value gets transformed into a decimal between 0 and 1	base R	within-sample	
global_min-max	☑	☑	For the whole matrix, the minimum value of gets transformed into a 0, the maximum value gets transformed into a 1, and every other value gets transformed into a decimal between 0 and 1	base R	across-sample and within-sample	
LogNormalize	☑	☑	Feature counts for each cell/sample are divided by the total counts for that cell/sample and multiplied by the scale.factor. This is then natural-log transformed using log1p**(this method has also log-tranform incorporated)**	Seurat package	across-sample and within-sample	
Quantile Normalisation (QN)-**(only in the pipeline)**	☑	☑	normalization based upon quantiles(first used in microarrays)	preprocessCore	across-sample and within-sample	
Trimmed Mean of M Values(TMM)	☑	☑	uses a weighted trimmed mean of the log expression ratios between samples	EdgeR	across-sample and within-sample	
Upper Quantile(UQ)**(only in the pipeline)**		☑	Upper Quartile normalization divides each count by the 75th percentile of the counts in its sample.	DESeq2	across-sample and within-sample	
DESEq2's median ratios**(only in the pipeline)**		☑	counts divided by sample-specific size factors determined by median ratio of gene counts relative to geometric mean per gene	DESeq2	across-sample	
SCTransform **(only in the pipeline)**	☑		Normalization and variance stabilization of single-cell RNA-seq data using regularized negative binomial regression(vst transformation included)	R package sctransform (github. com/ChristophH/sctransform)		
scater**(only in the pipeline)**	☑		Compute (normalized expression values by dividing counts for each cell by the corresponding size factor.	scater package Bioconductor		
scran	☑		The scran method uses a deconvolution approach that partitions cells into pools, normalizes across cells in each pool, then uses the resulting system of linear equations to define individual cell factors.	scran package		
Linnorm **(only in the pipeline)**	☑		Linnorm assumes that a set of genes are homogeneously (stably) expressed across different cells/samples. The Linnorm algorithm calculates normalization and transformation parameters by utilizing these stably expressed genes. After normalization and transformation, these genes will have: (i) stable expression values and (ii) approach homoscedasticity and normality. Hence, Linnorm's first step is to identify the stable genes by filtering. After calculating the parameters with the stable genes, the parameters are applied to the entire dataset. All zeroes in each gene are ignored in the following steps.	Linnorm package		